

Delaval, Jan

123453

From: Gambel, Phillip
Sent: Monday, June 07, 2004 9:21 AM
To: Delaval, Jan
Subject: sequence search for 09/ 816,697

jan

please perform a sequence and a sequence interference search

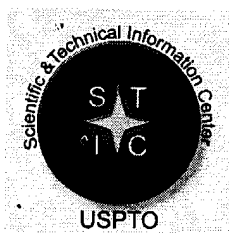
09/ 816,697

SEQ ID NO: 2 (lorenz slic)

thanx

phillip gambel
at unit 1644
272-0844

1644 maiblox 3c70



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 123953

TO: Phillip Gambel
Location: 3e81 / 3c70
Monday, June 07, 2004
Art Unit: 1644
Phone: 272-0844
Serial Number: 09 / 816697

From: Jan Delaval
Location: Biotech-Chem Library
Rem 1A51
Phone: 272-2504

jan.delaval@uspto.gov

Search Notes

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Att Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg Room Location: _____ Results Format Preferred (enter: PAPER DISK E-MAIL): _____

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept of novelty in the invention. Define any terms that may have a special meaning. Give examples of relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____
 Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY

Searcher _____	Type of Search	Vendors and cost where applicable
Searcher Phone #. 22504	NA Sequence (#) _____	STN _____
Searcher Location _____	AA Sequence (#) <input checked="" type="checkbox"/>	Dialog _____
Date Searcher Picked Up 6/7	Structure (#) _____	Questel/Orbit _____
Date Completed: 6/7	Bibliographic _____	Dr. Link _____
Searcher Prep & Review Time _____	Litigation _____	Lexis/Nexis _____
General Prep Time 60	Fulltext _____	Sequence Systems <input checked="" type="checkbox"/>
Online Time 40	Patent Family _____	WWW/Internet _____
	Other _____	Other (specify) _____

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OM protein - protein search, using sw model

Run on: June 7, 2004, 09:29:08 ; Search time 18 Seconds

(without alignments)

314.120 Million cell updates/sec

Title: US-09-816-697A-2

Perfect score: 1650

Sequence: 1 MASPEHPGPGCMGPITQCT.....RRTPRGITLKEITVREYLH 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1253.5	76.0	313	1 SNXK_MOUSE	Q9d2y5 mus musculus
2	413.5	25.1	373	1 SNXK_HUMAN	Q969t3 homo sapien
3	123	7.5	342	1 SNXF_HUMAN	Q9nrs6 homo sapien
4	118	7.2	169	1 SNXO_HUMAN	Q9y343 homo sapien
5	112.5	6.8	435	1 SNXR_HUMAN	Q96192 homo sapien
6	111	6.7	2477	1 SPNC_CHICK	P07751 gallus gall
7	102.5	6.2	1127	1 MDML_YEAST	Q01846 saccharomyc
8	102	6.2	2472	1 SPNC_RAT	P16086 rattus norv
9	100.5	6.1	343	1 SNXG_HUMAN	P57768 homo sapien
10	99.5	6.0	1068	1 DAM2_MOUSE	Q80u19 mus musculus
11	99	6.0	2472	1 SPNC_HUMAN	Q13813 homo sapien
12	98.5	6.0	204	1 SNXN_HUMAN	Q96193 homo sapien
13	98.5	6.0	705	1 SNY1_HUMAN	P17600 homo sapien
14	97	5.9	2702	1 SNXB_HUMAN	Q9y5w9 homo sapien
15	97	5.9	595	1 SNX9_MOUSE	Q91vh2 mus musculus
16	97	5.9	4684	1 PLE1_HUMAN	P17600 homo sapien
17	96.5	5.8	387	1 SNX7_HUMAN	Q9unh6 homo sapien
18	96	5.8	595	1 SNX9_HUMAN	Q9y5x1 homo sapien
19	95.5	5.8	339	1 NCF4_MOUSE	P97369 mus musculus
20	95.5	5.8	387	1 SNX7_MOUSE	Q9cy18 mus musculus
21	95.5	5.8	580	1 SRK1_SCHPO	Q94547 schizosacch
22	95	5.8	943	1 UVRA_UREPA	Q9pr42 ureaplasma
23	94.5	5.7	496	1 SGK3_MOUSE	Q9ere3 mus musculus
24	93.5	5.7	496	1 SGK3_HUMAN	Q96br1 homo sapien
25	92.5	5.6	450	1 SNX4_HUMAN	Q95219 homo sapien
26	92	5.6	706	1 SNY1_BOVIN	P17599 bos taurus
27	92	5.6	3674	1 SPCR_HUMAN	Q9nrc6 homo sapien
28	91.5	5.5	327	1 PKB6_MOUSE	Q9ixw8 mus musculus
29	91	5.5	1565	1 FBN6_HUMAN	O15061 homo sapien
30	90.5	5.5	193	1 SNXK_HUMAN	Q96194 homo sapien
31	90.5	5.5	344	1 SNXG_RAT	P57769 rattus norv
32	90	5.5	1446	1 TE18_PRRVA	P33479 pseudorabie
33	90	5.5	1461	1 TE18_PRRVF	P11675 pseudorabie

RESULT 1

SNXK_MOUSE

ID SNXK_MOUSE STANDARD; PRT; 313 AA.

AC Q9D2Y5;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DE 28-FEB-2003 (Rel. 41, Last annotation update)

GN Sorting nexin 20.

OS SNX20.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J;

RA Hong W.;

RT *A new member (SNX20) of the sorting nexin protein family.*;

RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cecum;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Hayashizaki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,

RA Hayashizaki Y.;

RT *Functional annotation of a full-length mouse cDNA collection.*;

RL Nature 409:685-690(2001).

CC -!- FUNCTION: May be involved in several stages of intracellular

CC trafficking (by similarity).

CC -!- SIMILARITY: Belongs to the sorting nexin family.

CC -!- SIMILARITY: Contains 1 phox homology (PX) domain.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

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CC or send an email to license@isb-sib.ch).

CC -----

CC -----

CC -----

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OM protein - protein search, using sw model

Run on: June 7, 2004, 09:29:08 ; Search time 45 Seconds

(without alignments)
2215.639 Million cell updates/sec

Title: US-09-816-697A-2

Perfect score: 1650

Sequence: 1 MASPEHPSGCMGPITQCT.....RRTPRGITLKELTVREYLH 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	1650	100.0	316	4	Q7Z614 homo sapien
2	1245.5	75.5	313	11	Q8CHQ3
3	517	31.3	129	4	Q8IVS9
4	264	16.0	184	4	Q8WY78
5	210	12.7	326	5	Q9VQ61
6	174.5	10.6	199	4	Q8WUR6
7	122.5	7.4	398	13	Q7T332
8	122	7.4	152	4	Q14612
9	122	7.4	337	11	Q91WE1
10	117	7.1	952	10	Q9XIM1
11	116	7.0	1010	3	Q9USN1
12	115.5	7.0	450	5	Q95RK3
13	115.5	7.0	646	5	Q8MKN4
14	115	7.0	248	16	Q8XSS5
15	114.5	6.9	531	5	Q9W486
16	113	6.8	169	11	Q9CRB0

17	111.5	6.8	1232	5	Q9UIQ7	Q9ulq7 caenorthabdi
18	111	6.7	473	13	Q90990	Q90990 gallus gall
19	110.5	6.7	577	10	Q941X3	Q941X3 oryza sativ
20	110	6.7	336	11	Q8BMQ5	Q8bmq5 mus musculu
21	109.5	6.6	581	11	Q8BX57	Q8bx57 mus musculu
22	109.5	6.6	582	11	Q91WB6	Q91wb6 mus musculu
23	108.5	6.6	652	16	Q828M0	Q828m0 streptomyce
24	107.5	6.5	519	11	Q80TZ1	Q80tz1 mus musculu
25	107.5	6.5	526	11	Q8K4T6	Q8k4t6 rattus norv
26	107.5	6.5	532	11	Q7TQL6	Q7tql6 mus musculu
27	107	6.5	441	16	Q88FT0	Q88ft0 pseudomonas
28	107	6.5	520	5	Q9VK31	Q9vk31 drosophila
29	106.5	6.5	539	11	Q8K4V4	Q8k4v4 rattus norv
30	106.5	6.5	579	11	Q7TNZ7	Q7tnz7 rattus norv
31	104.5	6.3	1065	10	Q8H7X9	Q8h7x9 oryza sativ
32	104	6.3	545	5	Q861F6	Q861f6 dictyosteli
33	103.5	6.3	1006	10	Q8S018	Q8s018 oryza sativ
34	103.5	6.3	1096	10	Q7X7B5	Q7x7b5 oryza sativ
35	102	6.2	1359	11	Q8K380	Q8k380 mus musculu
36	101.5	6.2	450	11	Q91YJ2	Q91yj2 mus musculu
37	101	6.1	1325	4	Q9UG16	Q9ug16 homo sapien
38	101	6.1	2452	4	Q7Z6M5	Q7z6m5 homo sapien
39	100.5	6.1	344	4	Q8N4U3	Q8n4u3 homo sapien
40	100.5	6.1	450	4	Q96CA3	Q96ca3 homo sapien
41	100.5	6.1	578	4	Q7Z7A4	Q7z7a4 homo sapien
42	99.5	6.0	515	4	Q96R07	Q96r07 homo sapien
43	99.5	6.0	649	4	Q9NKB8	Q9nkb8 homo sapien
44	99.5	6.0	1065	10	Q91WZ8	Q91wz8 oryza sativ
45	99	6.0	437	11	Q8CE50	Q8ce50 mus musculu

ALIGNMENTS

RESULT 1

Q7Z614 PRELIMINARY; PRT; 316 AA.

AC Q7Z614; Q7Z614; (TREMBLrel. 25, Created)

DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Selectin ligand interactor cytoplasmic-1.

GN SLIC1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Shih H.H., Lorenz M., Sako D., Bridges K., Kriz R., Shaw G.D.;

RT "SLIC-1: A Novel Sorting Nexin that Affects Subcellular Distribution

of PSG1-1.";

RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY302441; AAP58362.1; --

KW Lectin; Selectin

SQ SEQUENCE 316 AA; 36177 MW; 48D06CF4490907F4 CRC64;

Query Match 100.0%; Score 1650; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 4.3e-132;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASPEHPSGCMGPITQCTARTQOEAPATGPDLPHPGPDGHLDTGSLSSNMTREL 60

Db 1 MASPEHPSGCMGPITQCTARTQOEAPATGPDLPHPGPDGHLDTGSLSSNMTREL 60

Qy 61 QQYQWQKCKWKVKLLFETASARIEERKSKFVYVYQIIVITQSGFNNKAVLERYSD 120

Db 61 QQYQWQKCKWKVKLLFETASARIEERKSKFVYVYQIIVITQSGFNNKAVLERYSD 120

Qy 121 AKLQALKKTFREIEDEVEFPKHLTGNFAEMICERRALQEVYLGILYATRCVRRSREF 180

Db 121 AKLQALKKTFREIEDEVEFPKHLTGNFAEMICERRALQEVYLGILYATRCVRRSREF 180


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QY 181 LDFLTRPELRFAFGCLRAGQYPRALRLRLVLPLOEKLTAHCAPAAVPAALCAVLLCHRD 240
Db 181 LDFLTRPELRFAFGCLRAGQYPRALRLRLVLPLOEKLTAHCAPAAVPAALCAVLLCHRD 240
QY 241 DRPAFAAGGERALQRLQAREGHRYYPALLDAMVRLAYALGKDFVTLQERLEESQLRRPT 300
Db 241 DRPAFAAGGERALQRLQAREGHRYYPALLDAMVRLAYALGKDFVTLQERLEESQLRRPT 300
QY 301 PRGITLKELTVREYLH 316
Db 301 PRGITLKELTVREYLH 316

RESULT 2
Q8CHQ3 PRELIMINARY; PRT; 313 AA.
AC Q8CHQ3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE RIKEN CDNA 9130017C17 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Lung;
RA Strausberg R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC039809; AAH9809.1; -.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR InterPro; IPR001683; PX.
DR Pfam; PF00787; PX; 1.
DR SMART; SM00312; PX; 1.
DR PROSITE; PS0195; PX; 1.
SQ SEQUENCE 313 AA; 36018 MW; F1236D0A2521C34 CRC64;

Query Match 75.5%; Score 1245.5; DB 11; Length 313;
Best Local Similarity 77.1%; Pred. No. 1e-97;
Matches 243; Conservative 25; Mismatches 44; Indels 3; Gaps 1;

QY 1 MASPEHSGPGMGPICTOCTARTQOAPATGPDLPHPGPDGHLDTGSLSSNSMTTREL 60
Db 1 MASPEHSGPGMGPICTOCTARTQOAPATGPDLPHPGPDGHLDTGSLSSNSMTTREL 60
QY 61 QQYWNQKCRWKHVLLFFELASRIERKVKFVYQIIIVIQGTFDNNKAVLERYSD 120
Db 61 QQYWNQKCRWKHVLLFFELASRIERKVKFVYQIIIVIQGTFDNNKAVLERYSD 120
QY 121 AKLOKALLTFREITEDVFPKHLTGNTFABEMICERRALQYILGLLYAIRCVRRESREF 180
Db 121 AKLOKALLTFREITEDVFPKHLTGNTFABEMICERRALQYILGLLYAIRCVRRESREF 180
QY 178 LDFLTRPELRFAFGCLRAGQYPRALRLRLVLPLOEKLTAHCAPAAVPAALCAVLLCHRD 240
Db 178 LDFLTRPELRFAFGCLRAGQYPRALRLRLVLPLOEKLTAHCAPAAVPAALCAVLLCHRD 240
QY 241 DRPAFAAGGERALQRLQAREGHRYYPALLDAMVRLAYALGKDFVTLQERLEESQLRRPT 300
Db 241 DRPAFAAGGERALQRLQAREGHRYYPALLDAMVRLAYALGKDFVTLQERLEESQLRRPT 300
QY 301 PRGITLKELTVREYL 315
Db 301 PRGITLKELTVREYL 315

RESULT 3
Q8IV59 PRELIMINARY; PRT; 129 AA.
AC Q8IV59;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE RIKEN CDNA 9130017C17 gene.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC027944; AAH27944.1; -.
DR EMBL; BC027944; AAH27944.1; -.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR InterPro; IPR001683; PX.
DR PROSITE; PS0195; PX; 1.
SQ SEQUENCE 129 AA; 14186 MW; 7037F3ABC0033C43 CRC64;

Query Match 31.3%; Score 517; DB 4; Length 129;
Best Local Similarity 98.9%; Pred. No. 3e-36;
Matches 94; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASPEHSGPGMGPICTOCTARTQOAPATGPDLPHPGPDGHLDTGSLSSNSMTTREL 60
Db 1 MASPEHSGPGMGPICTOCTARTQOAPATGPDLPHPGPDGHLDTGSLSSNSMTTREL 60
QY 61 QQYWNQKCRWKHVLLFFELASRIERKVKFVY 95
Db 61 QQYWNQKCRWKHVLLFFELASRIERKVKFVY 95

RESULT 4
Q8WY78 PRELIMINARY; PRT; 184 AA.
AC Q8WY78;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE PF3993 (Hypothetical protein FLJ34040) (Hypothetical protein FLJ38532).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Qin W.X.; Zhou X.M.; Zhang P.P.; Jiang H.Q.; Huang Y.; Wan D.F.;
RA Gu J.R.;
RT "Novel human cDNA clones with function of inhibiting cancer cell growth."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Kawakami B.; Sugiyama A.; Takemoto M.; Sugiyama T.; Irie R.;
RA Osuki T.; Sato H.; Ota T.; Wakamatsu A.; Ishii S.; Yamamoto J.;
RA Isono Y.; Kawai-Hio Y.; Saito K.; Nishikawa T.; Kimura K.;
RA Yamashita H.; Matsumoto K.; Nakamura Y.; Sekine M.; Kikuchi H.; Kanda K.;
RA Wagatsuna M.; Murakawa K.; Kanehori K.; Takahashi-Fujii A.; Oshima A.;
RA Suzuki Y.; Sugano S.; Nagahara K.; Masuho Y.; Nagai K.; Isogai T.;
RT "NEDO human cDNA sequencing project."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF258570; AG23773.1; -.
DR EMBL; AK091359; BAC03646.1; -.
DR EMBL; AK095851; BAC04637.1; -.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR InterPro; IPR001683; PX.
DR PROSITE; PS0195; PX; 1.
SQ SEQUENCE 184 AA; 20612 MW; C3697FE2A1B19559 CRC64;

Query Match 16.0%; Score 264; DB 4; Length 184;
Best Local Similarity 37.3%; Pred. No. 1.5e-14;
Matches 69; Conservative 27; Mismatches 77; Indels 12; Gaps 3;
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2004, 09:29:07 ; Search time 59 Seconds
(without alignments)
1513.305 Million cell updates/sec

Title: US-09-816-697A-2

Perfect score: 1650

Sequence: 1 MASPEHPGSGMGPIQTCT.....RRTPRGITLXELTVREYLH 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A: Geneseq 23Jan04: *

- 1: Geneseqp1980s: *
- 2: Geneseqp1990s: *
- 3: Geneseqp2000s: *
- 4: Geneseqp2001s: *
- 5: Geneseqp2002s: *
- 6: Geneseqp2003as: *
- 7: Geneseqp2003bs: *
- 8: Geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1650	100.0	316	4	AAG79225 Amino aci
2	1650	100.0	316	6	AAO26235 MDDT rela
3	1650	100.0	316	6	ABO07143 Novel hum
4	1650	100.0	334	4	AAG79120 Amino aci
5	1640	99.4	316	7	ADC31008 Human nov
6	464	28.1	148	3	ABU43067 Human ORF
7	333	20.2	239	6	ABU11470 Human MDD
8	324	19.6	156	4	AAm89008 Human imm
9	264	16.0	184	5	AAO17131 Human can
10	264	16.0	184	7	ADB64274 Human pro
11	255	15.5	580	4	ABG27894 Novel hum
12	249	15.1	93	4	AAm84390 Human imm
13	185.5	11.2	295	4	ABBS5625 Drosophil
14	125.5	7.6	212	4	ABG23125 Novel hum
15	118	7.2	173	7	AAU17487 Novel sig
16	118	7.2	173	7	ADB94195 Human nov
17	114.5	6.9	431	4	ABBS5662 Drosophil
18	112.5	6.8	168	3	ABBS5187 Human sec
19	112.5	6.8	541	5	ABO08158 Human cyt
20	108.5	6.6	141	4	AAU17481 Novel sig
21	108.5	6.6	141	7	ADB94189 Human nov
22	107.5	6.5	166	4	ABG22895 Novel hum
23	107	6.5	441	6	ABU39601 Protein e
24	107	6.5	520	4	ABBS61499 Drosophil
25	103.5	6.3	245	4	ABG20248 Novel hum

26	103.5	6.3	320	4	ABG07654	Abg07654 Novel hum
27	102	6.2	2472	7	ADBS5351	Adbs5351 Rat Prote
28	100.5	6.1	344	5	AAE23382	Aae23382 Human int
29	100.5	6.1	577	4	AAE02775	Aae02775 Human PRO
30	100.5	6.1	578	5	ABB97328	Abb97328 Novel hum
31	99.5	6.0	156	4	ABG22890	Abg22890 Novel hum
32	99.5	6.0	649	4	AAAB5680	AAab5680 Novel pro
33	99.5	6.0	705	4	AAAM39328	AAam39328 Human pol
34	99.5	6.0	714	4	AAAM1114	AAam1114 Human pol
35	99	6.0	141	4	AAAU17470	AAau17470 Novel sig
36	99	6.0	141	7	ADB94178	Adb94178 Human nov
37	99	6.0	2472	7	ADBS5353	Adbs5353 Human Pro
38	99	6.0	2477	7	ABR84742	ABr84742 Human spe
39	98.5	6.0	66	4	AAU17617	AAu17617 Novel sig
40	98.5	6.0	66	7	ADB94325	ADB94325 Human nov
41	98.5	6.0	165	4	AAU17438	AAu17438 Novel sig
42	98.5	6.0	165	7	ADB94146	Adb94146 Human nov
43	98	5.9	278	4	AAU17486	AAu17486 Novel sig
44	98	5.9	278	7	ADB94194	ADB94194 Human nov
45	98	5.9	585	4	ABB62665	Abb62665 Drosophil

ALIGNMENTS

RESULT 1

AAG79225

ID AAG79225 standard; protein; 316 AA.

XX AAG79225;

XX AC AAG79225;

XX DT 03-JAN-2002 (first entry)

XX DE Amino acid sequence of a human PSGL-1 binding protein.

XX KW Human; P-selectin glycoprotein ligand binding protein;

XX KW PSGL-1 binding protein; selectin ligand interactor cytoplasmic-1 protein;

XX KW SLIC-1 protein; signal transduction; cytoskeletal organization;

XX KW immune response; inflammatory response; cell adhesion; cell migration;

XX KW cell activation; cell growth; cell differentiation; cell proliferation;

XX KW immune system disorder; cardiovascular disorder; haematopoietic disorder;

XX KW thrombotic disorder.

XX OS Homo sapiens.

XX PN WO200173028-A2.

XX PD 04-OCT-2001.

XX PF 23-MAR-2001; 2001WO-US009469.

XX PR 24-MAR-2000; 2000US-0192104P.

XX PA (GENY) GENETICS INST INC.

XX PI Lorenz M, Kriz R, Weich N, Shaw GD;

XX DR WPI; 2001-616502/71.

XX DR N-PSDB; AA165832.

XX XX Isolated polynucleotides (SLIC-1) which encode novel P-selectin

XX glycoprotein ligand (PSGL-1) binding protein, useful as targets for

XX developing modulating agents to regulate a variety of cellular processes

XX including signal transduction.

XX Claim 14; Fig 1; 108pp; English.

XX PS The present sequence represents a human P-selectin glycoprotein ligand

XX (PSGL-1) binding protein. The protein is a member of the selectin ligand

XX interactor cytoplasmic (SLIC-1) family. The SLIC-1 polynucleotides and

XX polypeptides are useful as targets for developing modulating agents to

XX regulate a variety of cellular processes such as signal transduction, and

XX cytoskeletal organization, immune and inflammatory responses, inter- and

CC intra-cellular communication, adhesion, migration, cell activation,
 CC growth, differentiation and proliferation. The SLIC-1 proteins provide
 CC novel diagnostic targets and therapeutic agents to control or modulate
 CC SLIC-1 molecule-associated disorders such as an inflammatory or immune
 CC system disorder, a cardiovascular disorder, a cellular proliferation,
 CC activation, adhesion, growth, differentiation or migration disorder or a
 CC haematopoietic or thrombotic disorder
 XX
 SQ Sequence 316 AA;

Query Match 100.0%; Score 1650; DB 4; Length 316;
 Best Local Similarity 100.0%; Pred. No. 5.7e-163;
 Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASPEHFGSPGCMGPIITQCTARTQOEAPATGPDLPHPGDPGHLOTHSGLSNSSMTREL 60
 DB 1 MASPEHFGSPGCMGPIITQCTARTQOEAPATGPDLPHPGDPGHLOTHSGLSNSSMTREL 60
 QY 61 QQYWNQKCRKWKHVKLLFEIASARIEERKVKSVVYQIIIVITQSGFNNKAVLRRYSDF 120
 DB 61 QQYWNQKCRKWKHVKLLFEIASARIEERKVKSVVYQIIIVITQSGFNNKAVLRRYSDF 120
 QY 121 AKQKALLKTFREIEDVEFPKRLTGNFAEMICERRALQOEYLGLLYAIRCVRRESREF 180
 DB 121 AKQKALLKTFREIEDVEFPKRLTGNFAEMICERRALQOEYLGLLYAIRCVRRESREF 180
 QY 181 LDFLTRPELRAFCIRAGQYPRALELLRLVLPLOEKLTAHCPCAAVPAALCAVLLCHRD 240
 DB 181 LDFLTRPELRAFCIRAGQYPRALELLRLVLPLOEKLTAHCPCAAVPAALCAVLLCHRD 240
 QY 241 DRPAEAPAGGERALQRLQAREGHRYAPLDDAMVRLAYALGKOPVTQLERLESQLRPT 300
 DB 241 DRPAEAPAGGERALQRLQAREGHRYAPLDDAMVRLAYALGKOPVTQLERLESQLRPT 300
 QY 301 PRGITLKELTVREYLH 316
 DB 301 PRGITLKELTVREYLH 316

RESULT 2

AAO26235 ID AAO26235 standard; protein; 316 AA.

AC AAO26235;

DC 10-APR-2003 (first entry)

DE MDDT related human protein SEQ ID No 13.

KW Cytostatic; antiatherosclerotic; osteopathic; antiarteriosclerotic;
 KW hepatotropic; antipsoriatic; antiallergic; antianaemic; antiasthmatic;
 KW antithyroid; antiinflammatory; antihelminthic; antidiabetic; nephrotropic;
 KW ophthalmological; immunosuppressive; dermatological; antiulcer;
 KW antirheumatic; antiarthritic; antibacterial; virucide; fungicide;
 KW antiparasitic; protozoacide; tranquiliser; vulnerary; anti-HIV;
 KW neurotropic; neuroprotective; anticonvulsant; cerebroprotective;
 KW immunoleptic; molecules for disease detection and treatment; MDDT;
 KW neurogen; cancer; actinic keratosis; arteriosclerosis; atherosclerosis;
 KW bursitis; cirrhosis; hepatitis; psoriasis; AIDS; rheumatoid arthritis;
 KW adult respiratory distress syndrome; Addison's disease; allergy; anaemia;
 KW asthma; osteoporosis; autoimmune; haemolytic anaemia; scleroderma;
 KW autoimmune thyroiditis; Crohn's disease; atopic dermatitis;
 KW diabetes mellitus; Graves' disease; glomerulonephritis;
 KW systemic lupus erythematosus; systemic sclerosis; ulcerative colitis;
 KW haemodialysis; uveitis; trauma; Alzheimer's; Pick disease;
 KW Parkinson disease; amyotrophic lateral sclerosis; epilepsy; stroke;
 KW Huntington's disease; multiple sclerosis; dementia;
 KW extrapyramidal disorder; motor neuron disorder; central nervous system;
 KW neuromuscular disorder; metabolic; endocrine; toxic myopathy;
 KW periodic paralysis; mental disorder; human.

XX Homo sapiens.

PN

WO200296951-A1.

XX 05-DEC-2002.

PF 24-MAY-2002; 2002WO-US016676.

XX 25-MAY-2001; 2001US-0293723P.

PR 01-JUN-2001; 2001US-0295257P.

PR 08-JUN-2001; 2001US-0297220P.

PR 21-JUN-2001; 2001US-0300526P.

PR 29-JUN-2001; 2001US-0301874P.

PR 22-FEB-2002; 2002US-0359413P.

XX (INCY-) INCYTE GENOMICS INC.

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WO200296951-A1.

XX 05-DEC-2002.

PF 24-MAY-2002; 2002WO-US016676.

XX 25-MAY-2001; 2001US-0293723P.

PR 01-JUN-2001; 2001US-0295257P.

PR 08-JUN-2001; 2001US-0297220P.

PR 21-JUN-2001; 2001US-0300526P.

PR 29-JUN-2001; 2001US-0301874P.

PR 22-FEB-2002; 2002US-0359413P.

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WO200296951-A1.

XX 05-DEC-2002.

PF 24-MAY-2002; 2002WO-US016676.

XX 25-MAY-2001; 2001US-0293723P.

PR 01-JUN-2001; 2001US-0295257P.

PR 08-JUN-2001; 2001US-0297220P.

PR 21-JUN-2001; 2001US-0300526P.

PR 29-JUN-2001; 2001US-0301874P.

PR 22-FEB-2002; 2002US-0359413P.

XX (INCY-) INCYTE GENOMICS INC.

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WO200296951-A1.

XX 05-DEC-2002.

PF 24-MAY-2002; 2002WO-US016676.

XX 25-MAY-2001; 2001US-0293723P.

PR 01-JUN-2001; 2001US-0295257P.

PR 08-JUN-2001; 2001US-0297220P.

PR 21-JUN-2001; 2001US-0300526P.

PR 29-JUN-2001; 2001US-0301874P.

PR 22-FEB-2002; 2002US-0359413P.

XX (INCY-) INCYTE GENOMICS INC.

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OM protein - protein search, using sw model

Run on: June 7, 2004, 09:31:58 ; Search time 48 Seconds
(without alignments)
1852.146 Million cell updates/sec

Title: US-09-816-697A-2
Perfect score: 1650
Sequence: 1 MASPEHPGSPGCMGPITQCT.....RR2PRGITLKELTVREYLH 315

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters: 1155919

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1650	100.0	316	9	US-09-816-697-2
2	1650	100.0	316	15	US-10-161-927-64
3	1650	100.0	334	14	US-10-240-046A-5
4	1134	68.7	222	14	US-10-029-386-32848
5	264	16.0	184	15	US-10-104-047-2428
6	264	16.0	184	15	US-10-108-260A-3381
7	118	7.2	173	9	US-09-764-868-1052
8	112.5	6.8	344	12	US-10-112-944-322
9	112.5	6.8	541	12	US-10-415-187-2
10	108.5	6.6	141	9	US-09-764-868-1046
11	108.5	6.6	652	14	US-10-156-761-14177
12	107	6.5	441	12	US-10-282-122A-67525
13	103.5	6.3	387	16	US-10-408-765A-1906
14	102.5	6.2	443	15	US-10-369-493-1843
15	101.5	6.2	732	12	US-10-425-114-56615

16	100.5	6.1	344	16	US-10-399-455-9	Sequence 9, Appli
17	99.5	6.0	515	16	US-10-408-765A-2323	Sequence 2323, Ap
18	99.5	6.0	696	14	US-10-122-805-4	Sequence 4, Appli
19	99	6.0	141	9	US-09-764-868-1035	Sequence 1035, Ap
20	99	6.0	2477	14	US-10-360-053-28	Sequence 28, Appl
21	99	6.0	2477	16	US-10-408-765A-238	Sequence 238, App
22	98.5	6.0	66	9	US-09-764-868-1182	Sequence 1182, Ap
23	98.5	6.0	165	9	US-09-764-868-1003	Sequence 1003, Ap
24	98	5.9	278	9	US-09-764-868-1051	Sequence 1051, Ap
25	97	5.9	270	15	US-10-168-659-6	Sequence 6, Appli
26	97	5.9	395	15	US-10-080-334-246	Sequence 246, App
27	97	5.9	595	15	US-10-080-334-247	Sequence 247, App
28	96.5	5.8	447	14	US-10-106-638-4948	Sequence 4948, Ap
29	96.5	5.8	455	12	US-10-276-774-1983	Sequence 1983, Ap
30	96	5.8	441	12	US-10-282-122A-66398	Sequence 66398, A
31	96	5.8	595	12	US-10-170-385-319	Sequence 319, App
32	95.5	5.8	259	14	US-10-233-131-18	Sequence 18, Appl
33	95.5	5.8	259	15	US-10-240-145-70	Sequence 70, Appl
34	95.5	5.8	576	15	US-10-369-493-22712	Sequence 22712, A
35	95.5	5.8	1911	12	US-10-220-955-24	Sequence 24, Appl
36	95.5	5.8	2392	16	US-10-408-765A-1880	Sequence 1880, Ap
37	95.5	5.8	2930	10	US-09-957-837A-2	Sequence 2, Appli
38	95.5	5.8	3031	15	US-10-165-216-6	Sequence 6, Appli
39	95.5	5.8	3521	15	US-10-165-216-2	Sequence 2, Appli
40	95.5	5.8	3529	15	US-10-165-216-8	Sequence 8, Appli
41	95.5	5.8	3657	15	US-10-165-216-10	Sequence 10, Appl
42	95	5.8	608	14	US-10-204-887-87	Sequence 87, Appl
43	95	5.8	943	12	US-10-282-122A-76714	Sequence 76714, A
44	94.5	5.7	1049	12	US-10-168-582-7	Sequence 7, Appli
45	94.5	5.7	1049	14	US-10-317-835-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1

US-09-816-697-2

; Sequence 2, Application US/09816697

; Patent No. US20020037840A1

; GENERAL INFORMATION:

; APPLICANT: Lorenz, M., et al.

; TITLE OF INVENTION: A NOVEL P-SELECTIN GLYCOPROTEIN LIGAND (PSGL-1)

; FILE REFERENCE: BINDING PROTEIN AND USES THEREFOR

; CURRENT APPLICATION NUMBER: US/09/816,697

; PRIOR FILING DATE: 2001-03-23

; PRIOR FILING DATE: 60/192,104

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; TYPE: PRT

; LENGTH: 316

; ORGANISM: Homo sapiens

; US-09-816-697-2

Query Match 100.0%; Score 1650; DB 9; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.2e-151;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MASPEHPGSPGCMGPITQCTARTQOAPATGPDLPHPGPGHLDTHSGLSNSMTTREL	60
Db	1	MASPEHPGSPGCMGPITQCTARTQOAPATGPDLPHPGPGHLDTHSGLSNSMTTREL	60
Qy	61	QQYWNQKCRKWKVLLFEIASARIERKVKVWVQIIVIQGSPNNKAVLERRYSDF	120
Db	61	QQYWNQKCRKWKVLLFEIASARIERKVKVWVQIIVIQGSPNNKAVLERRYSDF	120
Qy	121	AKLQKALLTFREIEDEVEFPKHLTGNAFEMICERRALQYGLLYAIRCVRRSREF	180
Db	121	AKLQKALLTFREIEDEVEFPKHLTGNAFEMICERRALQYGLLYAIRCVRRSREF	180
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Db 181 LDFLTRPELREAFGCLRAGQYPRALELLRLVLPLOEKLTAHCPAAAVPALCAVLLCHRD 240
Qy 241 DRPAEFAAGERALQRLQAREGHRYYPALDAMVRLAYALGKDFVTLQERLEESQLRRPT 300
Db 241 DRPAEFAAGERALQRLQAREGHRYYPALDAMVRLAYALGKDFVTLQERLEESQLRRPT 300
Qy 301 PRGITLKELTVREYLH 316
Db 301 PRGITLKELTVREYLH 316

RESULT 2

US-10-161-927-64

; Sequence 64, Application US/10161927

; Publication No. US20030235821A1

; GENERAL INFORMATION:

; APPLICANT: Zerhusen, Bryan D.

; APPLICANT: Kekuda, Rameesh

; APPLICANT: Spytek, Kimberly A.

; APPLICANT: Shenoy, Suresh G.

; APPLICANT: Miller, Charles E.

; APPLICANT: Hjalte, Tord

; APPLICANT: Gerlach, Valerie L.

; APPLICANT: Baumgartner, Jason C.

; APPLICANT: Guo, Xiaojia

; APPLICANT: Gangolli, Esha A.

; APPLICANT: Vernet, Corine

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Li, Li

; APPLICANT: Pena, Carol E.A.

; APPLICANT: Gorman, Linda

; APPLICANT: Anderson, David W.

; APPLICANT: Edinger, Shlomit R.

; APPLICANT: Patturajan, Meera

; APPLICANT: Stone, David J.

; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS

; FILE REFERENCE: THE SAME

; FILE REFERENCE: 21402-377 D (Cura 577 Other)

; CURRENT APPLICATION NUMBER: US/10/161.927

; CURRENT FILING DATE: 2002-06-03

; PRIOR APPLICATION NUMBER: 60/295,661

; PRIOR FILING DATE: 2001-06-04

; PRIOR APPLICATION NUMBER: 60/295,607

; PRIOR FILING DATE: 2001-06-04

; PRIOR APPLICATION NUMBER: 60/296,404

; PRIOR FILING DATE: 2001-06-06

; PRIOR APPLICATION NUMBER: 60/296,418

; PRIOR FILING DATE: 2001-06-06

; PRIOR APPLICATION NUMBER: 60/296,575

; PRIOR FILING DATE: 2001-06-07

; PRIOR APPLICATION NUMBER: 60/297,414

; PRIOR FILING DATE: 2001-06-11

; PRIOR APPLICATION NUMBER: 60/297,567

; PRIOR FILING DATE: 2001-06-12

; PRIOR APPLICATION NUMBER: 60/298,528

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/325,685

; PRIOR FILING DATE: 2001-09-27

; PRIOR APPLICATION NUMBER: 60/299,133

; PRIOR FILING DATE: 2001-06-18

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 190

; SEQ ID NO 64

; LENGTH: 3-6

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-161-927-64

Query Match 100.0%; Score 1650; DB 15; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.2e-151;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MASPEHPGSPGCMGPITQCTARTQOEAPATGPDLPHPGPDGHLDTSGLSNSSMTTREL 60
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Db 61 QOYWQNKCRWKHKVLLFEIASARIEERKVSFVYQIIVITQTSFNNKAVLERRYSDF 120
Qy 121 AKLOKALLKTFREEIEDVEFPKHLTGNAFAEMICERRALQEYLGLLYAIRCVRRSREF 180
Db 121 AKLOKALLKTFREEIEDVEFPKHLTGNAFAEMICERRALQEYLGLLYAIRCVRRSREF 180
Qy 181 LDFLTRPELREAFGCLRAGQYPRALELLRLVLPLOEKLTAHCPAAAVPALCAVLLCHRD 240
Db 181 LDFLTRPELREAFGCLRAGQYPRALELLRLVLPLOEKLTAHCPAAAVPALCAVLLCHRD 240
Qy 241 DRPAEFAAGERALQRLQAREGHRYYPALDAMVRLAYALGKDFVTLQERLEESQLRRPT 300
Db 241 DRPAEFAAGERALQRLQAREGHRYYPALDAMVRLAYALGKDFVTLQERLEESQLRRPT 300
Qy 301 PRGITLKELTVREYLH 316
Db 301 PRGITLKELTVREYLH 316

RESULT 3

US-10-240-046A-5

; Sequence 5, Application US/10240046A

; Publication No. US20030190639A1

; GENERAL INFORMATION:

; APPLICANT: HUGOT, JEAN-PIERRE

; APPLICANT: THOMAS, GILLES

; APPLICANT: ZOUALI, MOHAMED

; APPLICANT: LESAGE, SUZANNE

; APPLICANT: CHAMAILLARD, MATHIAS

; TITLE OF INVENTION: GENES INVOLVED IN INTESTINAL INFLAMMATORY DISEASES AND USE

; FILE REFERENCE: THEREOF

; FILE REFERENCE: 37991-0009

; CURRENT APPLICATION NUMBER: US/10/240,046A

; CURRENT FILING DATE: 2003-04-02

; PRIOR APPLICATION NUMBER: PCT/FR 01/00935

; PRIOR FILING DATE: 2001-03-27

; PRIOR APPLICATION NUMBER: FR 00/03832

; PRIOR FILING DATE: 2000-03-27

; NUMBER OF SEQ ID NOS: 90

; SOFTWARE: Patent in Ver. 2.1

; SEQ ID NO 5

; LENGTH: 334

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-240-046A-5

Query Match 100.0%; Score 1650; DB 14; Length 334;
Best Local Similarity 100.0%; Pred. No. 1.3e-151;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASPEHPGSPGCMGPITQCTARTQOEAPATGPDLPHPGPDGHLDTSGLSNSSMTTREL 60
Db 19 MASPEHPGSPGCMGPITQCTARTQOEAPATGPDLPHPGPDGHLDTSGLSNSSMTTREL 78
Qy 61 QOYWQNKCRWKHKVLLFEIASARIEERKVSFVYQIIVITQTSFNNKAVLERRYSDF 120
Db 79 QOYWQNKCRWKHKVLLFEIASARIEERKVSFVYQIIVITQTSFNNKAVLERRYSDF 138
Qy 121 AKLOKALLKTFREEIEDVEFPKHLTGNAFAEMICERRALQEYLGLLYAIRCVRRSREF 180
Db 139 AKLOKALLKTFREEIEDVEFPKHLTGNAFAEMICERRALQEYLGLLYAIRCVRRSREF 198
Qy 181 LDFLTRPELREAFGCLRAGQYPRALELLRLVLPLOEKLTAHCPAAAVPALCAVLLCHRD 240
Db 199 LDFLTRPELREAFGCLRAGQYPRALELLRLVLPLOEKLTAHCPAAAVPALCAVLLCHRD 258
Qy 241 DRPAEFAAGERALQRLQAREGHRYYPALDAMVRLAYALGKDFVTLQERLEESQLRRPT 300

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OM protein - protein search, using sw model

Run on: June 7, 2004, 09:29:08 ; Search time 22 Seconds
(without alignments)
741.537 Million cell updates/sec

Title: US-09-816-697A-2

Perfect score: 1650

Sequence: 1 MASPEHPGSPGCMGPITQCT.....RRPTRGITLKELTVREYLH 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 3

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
- 1: /cgn2_6/protdata/2/iaa/5A_COMB.pep.*
 - 2: /cgn2_6/protdata/2/iaa/5B_COMB.pep.*
 - 3: /cgn2_6/protdata/2/iaa/6A_COMB.pep.*
 - 4: /cgn2_6/protdata/2/iaa/6B_COMB.pep.*
 - 5: /cgn2_6/protdata/2/iaa/ECTUS_COMB.pep.*
 - 6: /cgn2_6/protdata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106	6.4	713	US-09-252-991A-32624	Sequence 32624, A
2	99.5	6.0	696	US-08-906-865-4	Sequence 4, Appli
3	99.5	6.0	696	US-09-129-668-4	Sequence 4, Appli
4	96	5.8	444	US-09-252-991A-11066	Sequence 31066, A
5	95.5	5.8	259	US-09-808-701A-18	Sequence 18, Appl
6	95.5	5.8	2930	US-09-417-822-2	Sequence 2, Appli
7	94.5	5.7	393	US-09-107-532A-4397	Sequence 4397, Ap
8	90	5.5	3072	US-09-413-814-93	Sequence 93, Appl
9	90	5.5	3079	US-09-413-814-80	Sequence 80, Appl
10	89	5.4	663	US-09-252-991A-30342	Sequence 30342, A
11	89	5.4	833	US-09-489-039A-9336	Sequence 9336, Ap
12	89	5.4	1201	US-09-252-991A-32259	Sequence 32259, A
13	88.5	5.4	430	US-09-489-039A-7580	Sequence 7580, Ap
14	88.5	5.4	533	US-09-252-991A-20347	Sequence 20347, A
15	87.5	5.3	340	US-09-134-000C-6526	Sequence 6526, Ap
16	87	5.3	391	US-09-489-039A-12724	Sequence 12724, A
17	87	5.3	674	US-09-134-000C-4004	Sequence 4004, Ap
18	85.5	5.2	522	US-08-625-322-2	Sequence 2, Appli
19	85	5.2	338	US-08-890-719-12	Sequence 12, Appl
20	85	5.2	523	US-09-252-991A-33001	Sequence 33001, A
21	84	5.1	486	US-08-821-355A-8	Sequence 8, Appli
22	84	5.1	486	US-09-003-687A-8	Sequence 8, Appli
23	84	5.1	486	US-09-136-605-8	Sequence 8, Appli
24	83	5.0	947	US-09-543-681A-6556	Sequence 6556, Ap
25	83	5.0	1326	US-09-688-188B-15	Sequence 15, Appl
26	83	5.0	1326	US-09-291-417D-15	Sequence 15, Appl
27	82.5	5.0	302	US-09-252-991A-21992	Sequence 21992, A

28	82.5	5.0	316	4	US-09-252-991A-29960	Sequence 29960, A
29	82.5	5.0	602	4	US-09-252-991A-30458	Sequence 30458, A
30	82.5	5.0	814	4	US-09-489-039A-12276	Sequence 12276, A
31	82	5.0	149	4	US-09-621-976-4165	Sequence 4165, Ap
32	82	5.0	309	4	US-09-252-991A-30651	Sequence 30651, A
33	82	5.0	346	4	US-09-252-991A-22101	Sequence 22101, A
34	82	5.0	2509	4	US-09-252-991A-16642	Sequence 16642, A
35	81.5	4.9	451	1	US-08-625-322-4	Sequence 4, Appli
36	81.5	4.9	644	4	US-09-198-452A-63	Sequence 63, Appl
37	81.5	4.9	1206	4	US-09-252-991A-19632	Sequence 19632, A
38	81.5	4.9	3433	4	US-09-091-501B-10	Sequence 10, Appl
39	81	4.9	287	1	US-08-622-353-7	Sequence 7, Appli
40	81	4.9	287	2	US-08-622-352A-9	Sequence 9, Appli
41	81	4.9	287	3	US-08-826-390-9	Sequence 9, Appli
42	81	4.9	689	4	US-09-252-991A-28711	Sequence 28711, A
43	81	4.9	816	2	US-08-533-306A-6	Sequence 6, Appli
44	81	4.9	816	2	US-08-742-923A-6	Sequence 6, Appli
45	81	4.9	818	4	US-09-134-000C-6355	Sequence 6355, Ap

ALIGNMENTS

RESULT 1

US-09-252-991A-32624

Sequence 32624, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

PRIOR FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 32624

LENGTH: 713

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-32624

Query Match 6.4%; Score 106; DB 4; Length 713;

Best Local Similarity 24.0%; Pred. No. 0.0092;

Matches 102; Conservative 41; Mismatches 132; Indels 150; Gaps 26;

QY 4 PEHPG-----SPGCMGPITQ-----CTATQOEAPATGPDLPHPGPDGHLD-----44

Db 18 PEPPGGIVASEGC-GSISMLEFGKVLSSLCRPLGQESG-----LPHSSCSGHDDEPAS 70

QY 45 -----TH-SGLSS--NSSMTTREIQYQWQKCRKWKVKI-----76

Db 71 RVKKEENQPRSEVRHLSGASSPRSLFSSGAVYPMENQS-----PHLSLRVPTTQCNLS 127

QY 77 -----LFEIASARIEERKVKFVVQIIVQITGSPDNKAVLERRYSDFAKLQ 124

Db 128 FCDATPKDQIKYWLHLPKANLGE---TARQLYQ-----GLIELNQLVPE---ARLQ 174

QY 125 KALLKTRERIEEDVFPKRHLTCNFAEMIC-ERRR-----ALOEVLGLLYAIRC- 174

Db 175 ---LLBLFRPE---VHFVCAHLRHFHLNQAIVLDERPKIANLCQALQNLHAIQYKLVVQ 229

QY 175 ---RESRELDLFT---RPELREAFG-CLRAGQ-----YPRALELLLRV 211

Db 230 EAPRNSRDRQAQLLVGICQAIRSLCGPLIFASQLYCPVEGLWLEHLQYQLASQGVHR 289

QY 212 LPLOEKLTAHCP-----AAAVPALCNVLLCHR-----DLDRPAEAFPAAGERALQRLQAR- 260

Db 290 LAVRDELAKHTPGLSVEQAYLPLILGCGARCQNMQRNNIARLAEVLEPNSQLLSIQSATL 349

QY 261 ECHRYA-PLIDAMV-----LAVAKGDF-----VTQRR-EESSQRRPTP 301
DB 350 PGSLFIAVPOIDGPPRYSLYPETQLANALGIDTQPLVELIREYLLQPEARAKARLEPLI 409
QY 302 RGITL 306
DB 410 EGVTL 414

RESULT 2

US-08-906-865-4
; Sequence 4, Application US/08906865
; Patent No. 6040168
; GENERAL INFORMATION:
; APPLICANT: Greengard, Paul
; APPLICANT: Porton, Barbara
; APPLICANT: Kao, Hung-Teh
; TITLE OF INVENTION: DNA ENCODING THE HUMAN SYNAPSIN III GENE
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/906,865
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 696 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: /desc = "Synapsin Ia"
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens

US-08-906-865-4

Query Match 6.0%; Score 99.5; DB 3; Length 696;

Best Local Similarity 25.0%; Pred. No. 0.048;

Matches 72; Conservative 29; Mismatches 96; Indels 91; Gaps 17;

QY 4 PEHPG--SPGCM-GRITQCTARTQOEAPATGPDLPHPGPDGHLDTGSLSSNMTTREL 60
DB 32 PPPGAHSPGATPGGTATERSGVAPASPAAPSGSGGGGFFSSLSNAVKQTT--- 88
QY 61 QQYWNQKCRWKHVLFEIASARIEBKVKFVVYQIIVITQGSFNNKA-----V 112
DB 89 -----AAAAATFSEQ-----VGGSGGAGRGGAASRVLLV 118
QY 113 LERRYSDFAKLOKALKTFREEI-----EDVEPR-----KHLTGNFAEMICERRALQY 164
DB 119 IDEPHTWAKYFKG--KTHGEIDIKVEQAEFSDNLVAHANGGFSVDMVELRN----- 170

QY 165 LGLLYAIRCVRRSREFLDF-LTRPELREAFGLRAGQVPRALELLRLVLPLOEKLTAHCP 223
DB 171 -----GVKVVRSUKP--DFVLIR---QHAFSMANGDY-RSL-----VIGLQ----- 206
QY 224 AAAPALCAVLLCHRDLDRAEPAAAGERALORLOAREGHRYVAPLLD 271
DB 207 YAGIPSVNLSHVSYNFCDKP-WVFAQVRLHKKLGTE-----PFLID 248

RESULT 3

US-09-129-668-4
; Sequence 4, Application US/09129668B
; Patent No. 6429010
; GENERAL INFORMATION:
; APPLICANT: Greengard, Paul
; APPLICANT: Porton, Barbara
; APPLICANT: Kao, Hung-Teh
; TITLE OF INVENTION: DNA ENCODING THE HUMAN SYNAPSIN III GENE AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 600-1-202 CIP
; CURRENT APPLICATION NUMBER: US/09/129,668B
; CURRENT FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 08/906,865
; EARLIER FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 4
; LENGTH: 696
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-129-668-4

Query Match 6.0%; Score 99.5; DB 4; Length 696;

Best Local Similarity 25.0%; Pred. No. 0.048;

Matches 72; Conservative 29; Mismatches 96; Indels 91; Gaps 17;

QY 4 PEHPG--SPGCM-GRITQCTARTQOEAPATGPDLPHPGPDGHLDTGSLSSNMTTREL 60
DB 32 PPPGAHSPGATPGGTATERSGVAPASPAAPSGSGGGGFFSSLSNAVKQTT--- 88
QY 61 QQYWNQKCRWKHVLFEIASARIEBKVKFVVYQIIVITQGSFNNKA-----V 112
DB 89 -----AAAAATFSEQ-----VGGSGGAGRGGAASRVLLV 118
QY 113 LERRYSDFAKLOKALKTFREEI-----EDVEPR-----KHLTGNFAEMICERRALQY 164
DB 119 IDEPHTWAKYFKG--KTHGEIDIKVEQAEFSDNLVAHANGGFSVDMVELRN----- 170
QY 165 LGLLYAIRCVRRSREFLDF-LTRPELREAFGLRAGQVPRALELLRLVLPLOEKLTAHCP 223
DB 171 -----GVKVVRSUKP--DFVLIR---QHAFSMANGDY-RSL-----VIGLQ----- 206
QY 224 AAAPALCAVLLCHRDLDRAEPAAAGERALORLOAREGHRYVAPLLD 271
DB 207 YAGIPSVNLSHVSYNFCDKP-WVFAQVRLHKKLGTE-----PFLID 248

RESULT 4

US-09-252-991A-31066
; Sequence 31066, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142